



## SEQUENCE LISTING

<110> Rieping, Mechthild

<120> A process for producing L-amino acids using strains of the  
Enterobacteriaceae family

<130> 7909/81000

<140> US/10/812,315

<141> 2004-03-30

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Artificial

<220>

<223> PCR Primer

<400> 1  
cacaatctag ataaaccata ttggaggga tc 32

<210> 2

<211> 25

<212> DNA

<213> Artificial

<220>

<223> PCR Primer

<400> 2  
gggaggaagc ttggggagat taatc 25

<210> 3<211> 1446

<212> DNA

<213> Escherichia coli

<220>

<221> DNA fragment

<222> (1)..(1446)

<223> PCR product

<220>

<221> CDS

<222> (33)..(1427)

<223> galP coding region

<400> 3  
cacaatctag ataaaccata ttggaggga tc atg cct gac gct aaa aaa cag 53  
Met Pro Asp Ala Lys Lys Gln  
1 5

ggg cgg tca aac aag gca atg acg ttt ttc gtc tgc ttc ctt gcc gct 101  
Gly Arg Ser Asn Lys Ala Met Thr Phe Phe Val Cys Phe Leu Ala Ala  
10 15 20

ctg gcg gga tta ctc ttt ggc ctg gat atc ggt gta att gct ggc gca 149  
Leu Ala Gly Leu Leu Phe Gly Leu Asp Ile Gly Val Ile Ala Gly Ala  
25 30 35

ctg ccg ttt att gca gat gaa ttc cag att act tcg cac acg caa gaa Leu Pro Phe Ile Ala Asp Glu Phe Gln Ile Thr Ser His Thr Gln Glu 40 45 50 55	197
tgg gtc gta agc tcc atg atg ttc ggt gcg gca gtc ggt gcg gtg ggc Trp Val Val Ser Ser Met Met Phe Gly Ala Ala Val Gly Ala Val Gly 60 65 70	245
agc ggc tgg ctc tcc ttt aaa ctc ggg cgc aaa aag agc ctg atg atc Ser Gly Trp Leu Ser Phe Lys Leu Gly Arg Lys Lys Ser Leu Met Ile 75 80 85	293
ggc gca att ttg ttt gtt gcc ggt tcg ctg ttc tct gcg gct gcg cca Gly Ala Ile Leu Phe Val Ala Gly Ser Leu Phe Ser Ala Ala Ala Pro 90 95 100	341
aac gtt gaa gta ctg att ctt tcc cgc gtt cta ctg ggg ctg gcg gtg Asn Val Glu Val Leu Ile Leu Ser Arg Val Leu Leu Gly Leu Ala Val 105 110 115	389
ggc gtc gcc tct tat acc gca cgc ctg tac ctc tct gaa att gcg ccg Gly Val Ala Ser Tyr Thr Ala Pro Leu Tyr Leu Ser Glu Ile Ala Pro 120 125 130 135	437
gaa aaa att cgt ggc agt atg atc tcg atg tat cag ttg atg atc act Glu Lys Ile Arg Gly Ser Met Ile Ser Met Tyr Gln Leu Met Ile Thr 140 145 150	485
atc ggg atc ctc ggt gct tat ctt tct gat acc gcc ttc agc tac acc Ile Gly Ile Leu Gly Ala Tyr Leu Ser Asp Thr Ala Phe Ser Tyr Thr 155 160 165	533
ggc gca tgg cgc tgg atg ctg ggt gtg att atc atc ccg gca att ttg Gly Ala Trp Arg Trp Met Leu Gly Val Ile Ile Ile Pro Ala Ile Leu 170 175 180	581
ctg ctg att ggt gtc ttc ttc ctg cca gac agc cca cgt tgg ttt gcc Leu Leu Ile Gly Val Phe Phe Leu Pro Asp Ser Pro Arg Trp Phe Ala 185 190 195	629
gcc aaa cgc cgt ttt gtt gat gcc gaa cgc gtg ctg cta cgc ctg cgt Ala Lys Arg Arg Phe Val Asp Ala Glu Arg Val Leu Leu Arg Leu Arg 200 205 210 215	677
gac acc agc gcg gaa gcg aaa cgc gaa ctg gat gaa atc cgt gaa agt Asp Thr Ser Ala Glu Ala Lys Arg Glu Leu Asp Glu Ile Arg Glu Ser 220 225 230	725
ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn 235 240 245	773
ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln 250 255 260	821
ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu 265 270 275	869
ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att Leu Ala Gly Tyr Thr Asn Thr Thr Glu Gln Met Trp Gly Thr Val Ile 280 285 290 295	917

gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt 965  
 Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val  
 300 305 310  
 gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg 1013  
 Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met  
 315 320 325  
 gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac 1061  
 Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His  
 330 335 340  
 tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att 1109  
 Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile  
 345 350 355  
 gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc 1157  
 Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser  
 360 365 370 375  
 gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act 1205  
 Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr  
 380 385 390  
 gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc 1253  
 Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr  
 395 400 405  
 atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct 1301  
 Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala  
 410 415 420  
 ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc 1349  
 Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr  
 425 430 435  
 aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt 1397  
 Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg  
 440 445 450 455  
 aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaag cttcctccc 1446  
 Lys Leu Arg Glu Ile Gly Ala His Asp  
 460

<210> 4  
 <211> 464  
 <212> PRT  
 <213> Escherichia coli

<400> 4  
 Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe  
 1 5 10 15  
 Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp  
 20 25 30  
 Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln  
 35 40 45  
 Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly  
 50 55 60  
 Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly  
 65 70 75 80

Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser  
 85 90 95  
 Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg  
 100 105 110  
 Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu  
 115 120 125  
 Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser  
 130 135 140  
 Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser  
 145 150 155 160  
 Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val  
 165 170 175  
 Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro  
 180 185 190  
 Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu  
 195 200 205  
 Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu  
 210 215 220  
 Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala  
 225 230 235 240  
 Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val  
 245 250 255  
 Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr  
 260 265 270  
 Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu  
 275 280 285  
 Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr  
 290 295 300  
 Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu  
 305 310 315 320  
 Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr  
 325 330 335  
 Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile  
 340 345 350  
 Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro  
 355 360 365  
 Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp  
 370 375 380  
 Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile  
 385 390 395 400  
 Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn  
 405 410 415  
 Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr  
 420 425 430

Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu  
435 440 445

Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp  
450 455 460